



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 8, 2017 – 09:00 AM EDT

PDB ID : 5JII  
Title : Crystal structure of human IgG1-Fc  
Authors : Humm, A.; Lobner, E.; Mlynek, G.; Obinger, C.; Djjinovic-Carugo, K.  
Deposited on : 2016-04-22  
Resolution : 1.79 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20029077  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029077

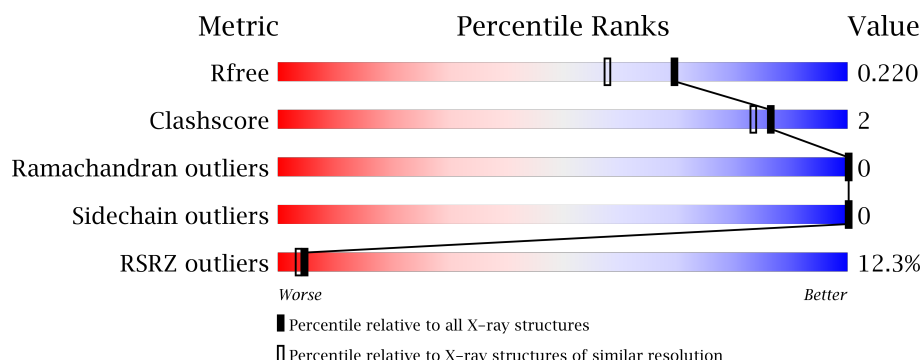
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.79 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	4827 (1.80-1.80)
Clashscore	112137	5742 (1.80-1.80)
Ramachandran outliers	110173	5676 (1.80-1.80)
Sidechain outliers	110143	5675 (1.80-1.80)
RSRZ outliers	101464	4906 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	222	<div> <div>11%</div> <div> <div></div> <div>88%</div> <div>5%</div> <div>7%</div> </div> </div>
1	B	222	<div> <div>12%</div> <div> <div></div> <div>89%</div> <div>5%</div> <div>6%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PO4	A	507	-	-	-	X
5	PO4	B	509	-	-	-	X
6	GOL	A	509	-	-	-	X
7	GAL	B	506	-	-	X	X

## 2 Entry composition [i](#)

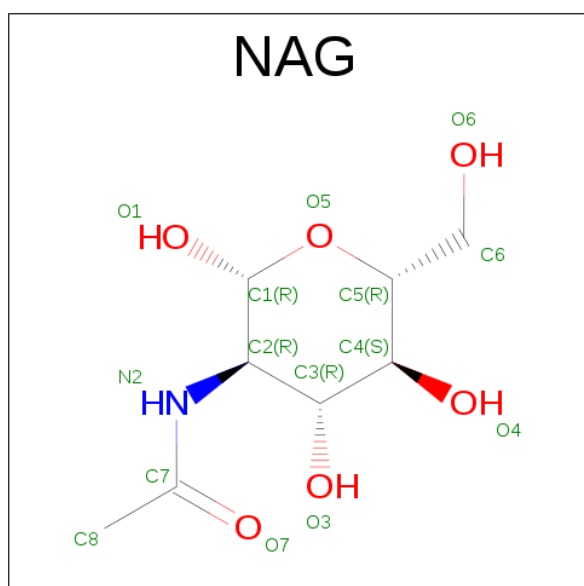
There are 9 unique types of molecules in this entry. The entry contains 7181 atoms, of which 3375 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Ig gamma-1 chain C region.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	207	Total	C	H	N	O	S	37	0	0
			3282	1056	1624	279	317	6			
1	B	208	Total	C	H	N	O	S	46	0	0
			3290	1059	1626	280	319	6			

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



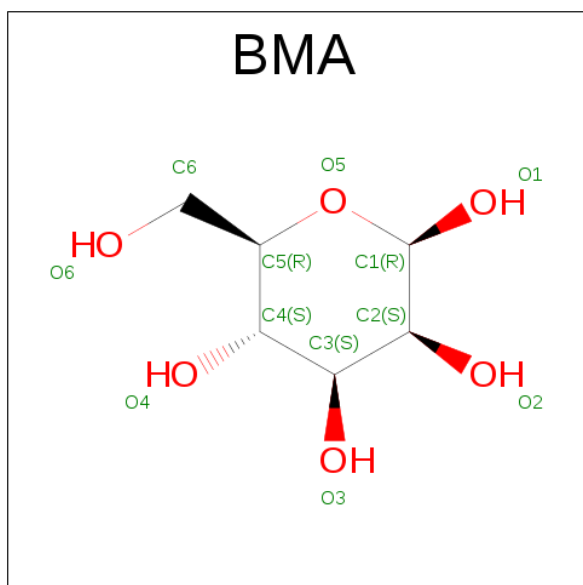
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O		0	0
			14	8	1	5			
2	A	1	Total	C	N	O		0	0
			14	8	1	5			
2	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
2	B	1	Total	C	H	N	O	0	0
			25	8	11	1	5		

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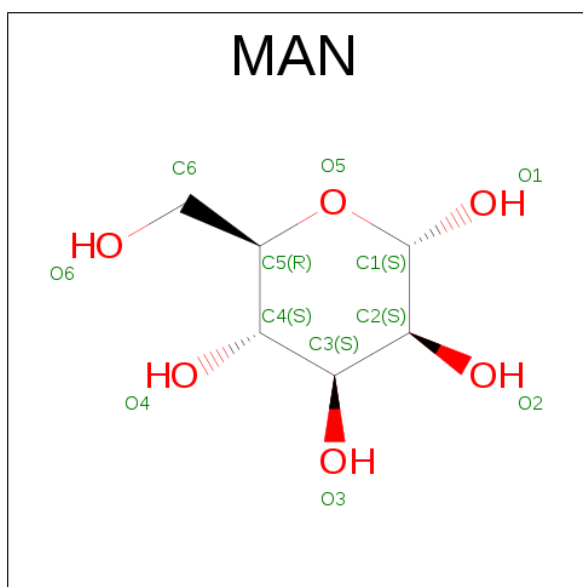
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
2	B	1	Total	C	H	N	O	0	0
			27	8	13	1	5		

- Molecule 3 is BETA-D-MANNOSE (three-letter code: BMA) (formula:  $C_6H_{12}O_6$ ).



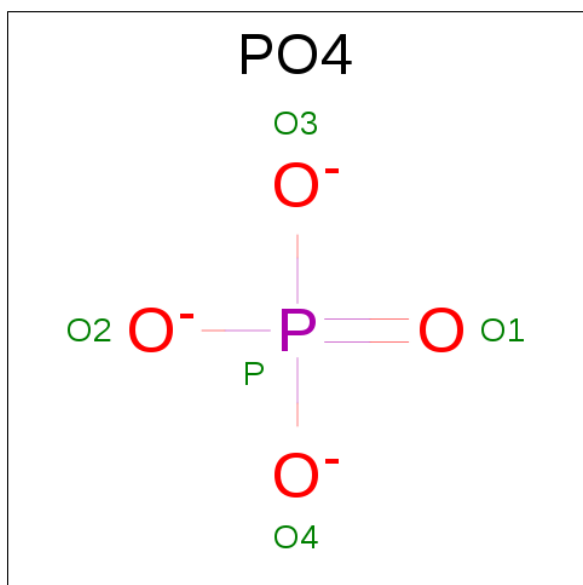
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O		0	0
			11	6	5			
3	B	1	Total	C	H	O	0	0
			20	6	9	5		

- Molecule 4 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula:  $C_6H_{12}O_6$ ).



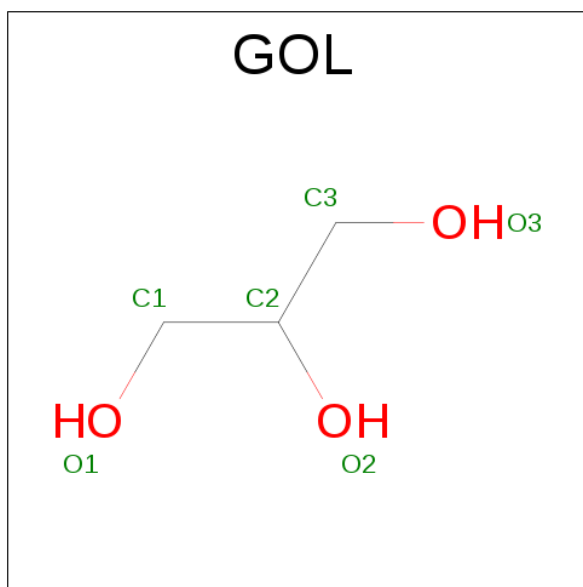
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			21	6	10	5		
4	A	1	Total	C	H	O	0	0
			22	6	11	5		
4	B	1	Total	C	H	O	0	0
			21	6	10	5		
4	B	1	Total	C	H	O	0	0
			22	6	11	5		

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



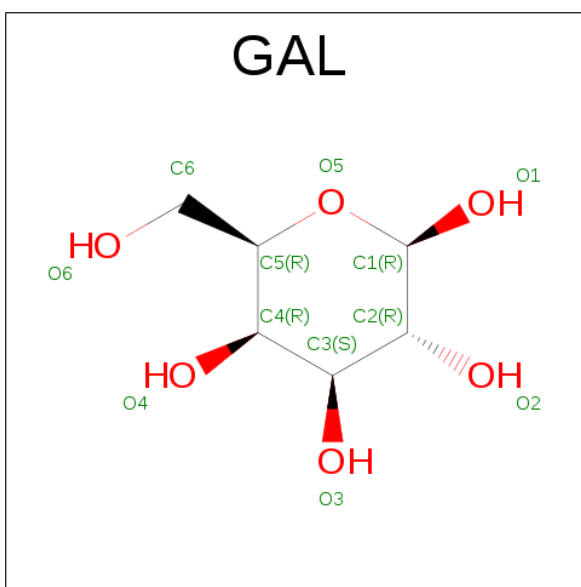
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			5	4	1		
5	B	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



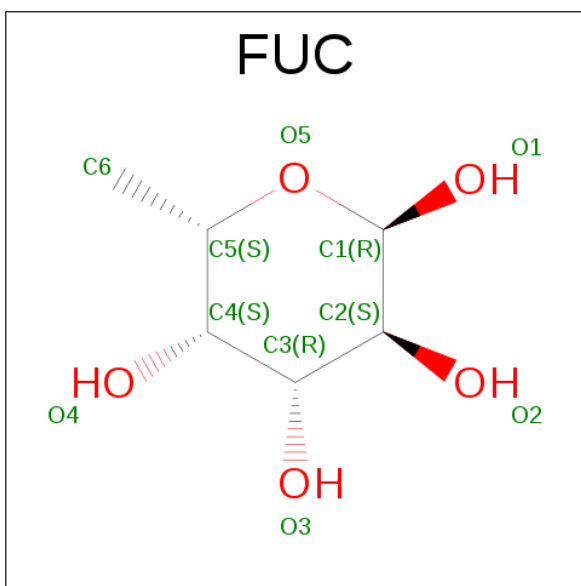
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			14	3	8	3		
6	A	1	Total	C	H	O	0	0
			14	3	8	3		
6	A	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 7 is BETA-D-GALACTOSE (three-letter code: GAL) (formula:  $C_6H_{12}O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			11	6	5		

- Molecule 8 is ALPHA-L-FUCOSE (three-letter code: FUC) (formula:  $C_6H_{12}O_5$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 9 is water.

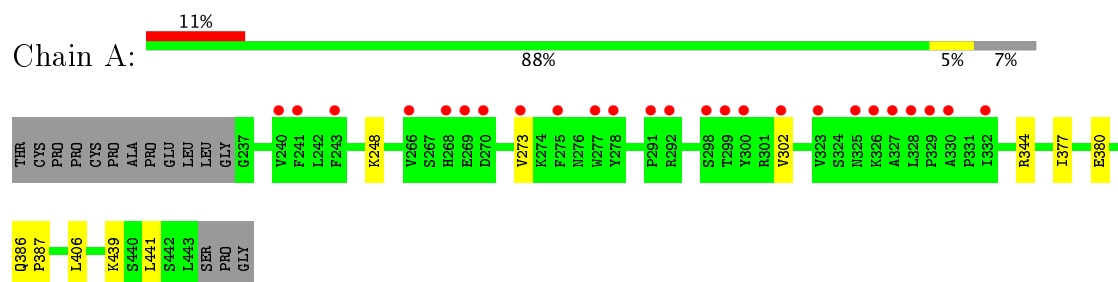


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	153	Total 153	O 153	0	0
9	B	132	Total 132	O 132	0	0

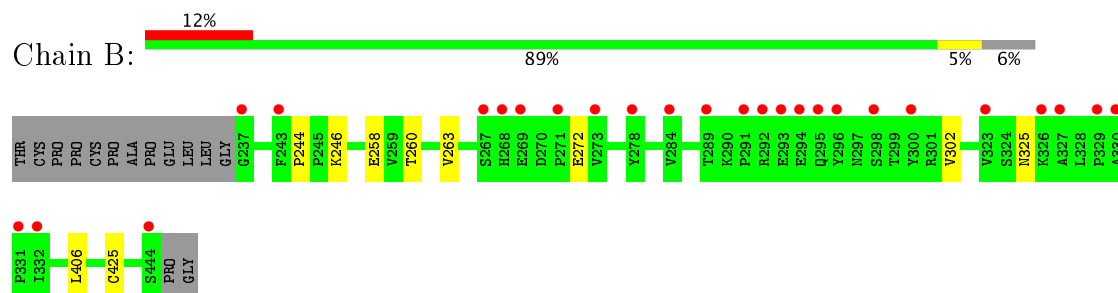
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Ig gamma-1 chain C region



- Molecule 1: Ig gamma-1 chain C region



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.38 Å 75.09 Å 149.40 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.89 – 1.79 46.89 – 1.79	Depositor EDS
% Data completeness (in resolution range)	97.8 (46.89-1.79) 97.8 (46.89-1.79)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.55 (at 1.79 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1894)	Depositor
R, $R_{free}$	0.181 , 0.221 0.179 , 0.220	Depositor DCC
$R_{free}$ test set	2652 reflections (5.09%)	DCC
Wilson B-factor (Å <sup>2</sup> )	28.8	Xtriage
Anisotropy	0.428	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 52.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7181	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.67% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, BMA, NAG, PO4, GAL, FUC, MAN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.64	0/1704	0.67	2/2322 (0.1%)
1	B	0.64	1/1710 (0.1%)	0.64	0/2330
All	All	0.64	1/3414 (0.0%)	0.66	2/4652 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	425	CYS	CB-SG	-6.84	1.70	1.82

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	344	ARG	NE-CZ-NH2	-5.99	117.30	120.30
1	A	441	LEU	CA-CB-CG	5.01	126.82	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1658	1624	1625	6	0
1	B	1664	1626	1630	9	0
2	A	42	13	37	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	42	37	35	0	0
3	A	11	0	8	0	0
3	B	11	9	8	0	0
4	A	22	21	19	0	0
4	B	22	21	19	0	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
6	A	18	24	24	2	0
7	B	11	0	10	7	0
8	B	10	0	10	0	0
9	A	153	0	0	2	1
9	B	132	0	0	1	1
All	All	3806	3375	3425	17	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (17) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:244:PRO:O	7:B:506:GAL:H5	1.81	0.81
1:B:272:GLU:O	1:B:325:ASN:ND2	2.24	0.70
1:B:246:LYS:HZ3	7:B:506:GAL:H3	1.58	0.68
1:B:246:LYS:NZ	7:B:506:GAL:H3	2.19	0.57
1:B:260:THR:OG1	7:B:506:GAL:H62	2.05	0.57
1:A:273:VAL:HG21	1:A:302:VAL:HG11	1.90	0.53
1:B:258:GLU:O	7:B:506:GAL:O6	2.29	0.50
1:A:248:LYS:NZ	1:A:380:GLU:OE2	2.35	0.49
1:A:386:GLN:HG3	1:A:387:PRO:HD2	1.97	0.46
1:B:406:LEU:C	1:B:406:LEU:HD12	2.37	0.44
6:A:508:GOL:H12	9:A:628:HOH:O	2.17	0.44
7:B:506:GAL:H3	9:B:702:HOH:O	2.17	0.43
1:B:246:LYS:NZ	7:B:506:GAL:C1	2.80	0.43
1:A:406:LEU:HD12	1:A:406:LEU:C	2.39	0.43
1:B:263:VAL:HB	1:B:302:VAL:HG22	2.02	0.42
1:A:439:LYS:HE3	9:A:651:HOH:O	2.20	0.41
1:A:377:ILE:HG23	6:A:508:GOL:H31	2.03	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:738:HOH:O	9:B:716:HOH:O[1_655]	2.17	0.03

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	205/222 (92%)	203 (99%)	2 (1%)	0	100	100
1	B	206/222 (93%)	204 (99%)	2 (1%)	0	100	100
All	All	411/444 (93%)	407 (99%)	4 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	193/205 (94%)	193 (100%)	0	100	100
1	B	194/205 (95%)	194 (100%)	0	100	100
All	All	387/410 (94%)	387 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	268	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

19 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	NAG	A	501	1,2	14,14,15	0.36	0	15,19,21	0.76	0
2	NAG	A	502	3,2	14,14,15	0.20	0	15,19,21	0.82	1 (6%)
3	BMA	A	503	2,4	11,11,12	1.30	2 (18%)	13,15,17	1.08	1 (7%)
4	MAN	A	504	3,2	11,11,12	0.85	0	13,15,17	1.03	1 (7%)
2	NAG	A	505	4	14,14,15	0.25	0	15,19,21	0.49	0
4	MAN	A	506	3	11,11,12	1.23	2 (18%)	13,15,17	1.19	1 (7%)
5	PO4	A	507	-	4,4,4	0.72	0	6,6,6	0.55	0
6	GOL	A	508	-	5,5,5	0.40	0	5,5,5	0.72	0
6	GOL	A	509	-	5,5,5	0.40	0	5,5,5	0.41	0
6	GOL	A	510	-	5,5,5	0.43	0	5,5,5	0.59	0
2	NAG	B	501	1,8,2	14,14,15	0.71	0	15,19,21	0.62	0
2	NAG	B	502	3,2	14,14,15	0.40	0	15,19,21	0.73	1 (6%)
3	BMA	B	503	2,4	11,11,12	1.35	3 (27%)	13,15,17	1.07	0
4	MAN	B	504	3,2	11,11,12	0.95	1 (9%)	13,15,17	1.48	3 (23%)
2	NAG	B	505	4,7	14,14,15	0.93	1 (7%)	15,19,21	1.14	1 (6%)
7	GAL	B	506	2	11,11,12	1.32	2 (18%)	13,15,17	2.43	3 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	MAN	B	507	3	11,11,12	0.98	0	13,15,17	1.01	0
8	FUC	B	508	2	9,10,11	0.68	0	13,14,16	1.04	0
5	PO4	B	509	-	4,4,4	0.77	0	6,6,6	0.32	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	501	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	502	3,2	-	0/6/23/26	0/1/1/1
3	BMA	A	503	2,4	-	0/2/19/22	0/1/1/1
4	MAN	A	504	3,2	-	0/2/19/22	0/1/1/1
2	NAG	A	505	4	-	0/6/23/26	0/1/1/1
4	MAN	A	506	3	-	0/2/19/22	0/1/1/1
5	PO4	A	507	-	-	0/0/0/0	0/0/0/0
6	GOL	A	508	-	-	0/4/4/4	0/0/0/0
6	GOL	A	509	-	-	0/4/4/4	0/0/0/0
6	GOL	A	510	-	-	0/4/4/4	0/0/0/0
2	NAG	B	501	1,8,2	-	0/6/23/26	0/1/1/1
2	NAG	B	502	3,2	-	0/6/23/26	0/1/1/1
3	BMA	B	503	2,4	-	0/2/19/22	0/1/1/1
4	MAN	B	504	3,2	-	0/2/19/22	0/1/1/1
2	NAG	B	505	4,7	-	0/6/23/26	0/1/1/1
7	GAL	B	506	2	-	0/2/19/22	0/1/1/1
4	MAN	B	507	3	-	0/2/19/22	0/1/1/1
8	FUC	B	508	2	-	0/0/17/20	0/1/1/1
5	PO4	B	509	-	-	0/0/0/0	0/0/0/0

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	503	BMA	O5-C1	-2.71	1.39	1.43
4	A	506	MAN	O5-C1	-2.31	1.39	1.43
3	B	503	BMA	C1-C2	2.15	1.57	1.52
3	B	503	BMA	C2-C3	2.16	1.55	1.52
4	B	504	MAN	C1-C2	2.20	1.57	1.52
7	B	506	GAL	C4-C5	2.32	1.58	1.53
3	A	503	BMA	C1-C2	2.38	1.57	1.52
7	B	506	GAL	O5-C5	2.50	1.48	1.43
3	A	503	BMA	C2-C3	2.62	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	505	NAG	C1-C2	2.72	1.56	1.52
4	A	506	MAN	C1-C2	2.75	1.58	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	504	MAN	O2-C2-C3	-3.63	103.04	110.17
4	A	506	MAN	O2-C2-C3	-3.32	103.65	110.17
4	A	504	MAN	O2-C2-C3	-2.90	104.47	110.17
2	B	502	NAG	C1-O5-C5	2.10	115.06	112.17
2	A	502	NAG	C1-O5-C5	2.18	115.16	112.17
3	A	503	BMA	O3-C3-C2	2.22	114.06	110.02
4	B	504	MAN	C1-O5-C5	2.33	115.38	112.17
7	B	506	GAL	O5-C1-C2	2.51	114.72	110.79
4	B	504	MAN	C1-C2-C3	2.76	113.15	109.65
2	B	505	NAG	O4-C4-C3	3.13	117.17	110.36
7	B	506	GAL	C1-O5-C5	4.94	118.97	112.17
7	B	506	GAL	C1-C2-C3	5.62	116.78	109.65

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	508	GOL	2	0
7	B	506	GAL	7	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å <sup>2</sup> )	Q<0.9
1	A	207/222 (93%)	0.75	25 (12%)	5 4	20, 45, 78, 93	5 (2%)
1	B	208/222 (93%)	0.73	26 (12%)	4 3	20, 42, 89, 107	6 (2%)
All	All	415/444 (93%)	0.74	51 (12%)	5 3	20, 44, 86, 107	11 (2%)

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	296	TYR	8.1
1	B	300	TYR	5.4
1	A	330	ALA	5.3
1	A	328	LEU	4.5
1	B	271	PRO	4.2
1	B	327	ALA	4.2
1	B	268	HIS	3.9
1	A	302	VAL	3.8
1	A	241	PHE	3.7
1	B	326	LYS	3.7
1	B	331	PRO	3.7
1	A	291	PRO	3.4
1	B	273	VAL	3.4
1	B	332	ILE	3.4
1	B	278	TYR	3.3
1	A	323	VAL	3.3
1	A	332	ILE	3.2
1	B	269	GLU	3.2
1	B	292	ARG	3.1
1	B	267	SER	3.0
1	A	326	LYS	2.9
1	B	295	GLN	2.7
1	A	329	PRO	2.7
1	B	298	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	323	VAL	2.7
1	A	277	TRP	2.7
1	B	294	GLU	2.6
1	A	299	THR	2.6
1	B	329	PRO	2.6
1	B	293	GLU	2.5
1	A	243	PHE	2.5
1	B	237	GLY	2.5
1	B	330	ALA	2.4
1	B	444	SER	2.4
1	A	240	VAL	2.4
1	B	284	VAL	2.4
1	B	243	PHE	2.4
1	A	275	PHE	2.3
1	A	278	TYR	2.3
1	A	298	SER	2.3
1	A	268	HIS	2.3
1	A	269	GLU	2.3
1	A	327	ALA	2.2
1	B	289	THR	2.2
1	A	292	ARG	2.2
1	A	325	ASN	2.2
1	A	300	TYR	2.1
1	A	270	ASP	2.1
1	A	266	VAL	2.1
1	A	273	VAL	2.0
1	B	291	PRO	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains.

The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
5	PO4	B	509	5/5	0.81	0.20	8.29	95,97,107,119	0
5	PO4	A	507	5/5	0.86	0.20	7.55	103,111,118,123	0
7	GAL	B	506	11/12	0.80	0.27	6.17	61,76,88,102	0
6	GOL	A	509	6/6	0.77	0.17	3.15	43,76,90,103	0
2	NAG	B	505	14/15	0.57	0.18	1.96	70,93,114,114	0
6	GOL	A	510	6/6	0.93	0.15	1.51	40,61,73,77	0
6	GOL	A	508	6/6	0.89	0.15	1.50	31,65,81,95	0
4	MAN	B	504	11/12	0.85	0.16	0.95	66,87,105,118	0
2	NAG	A	505	14/15	0.84	0.17	0.83	48,83,123,123	0
2	NAG	B	502	14/15	0.85	0.17	0.29	46,60,99,114	0
2	NAG	B	501	14/15	0.84	0.15	-0.38	53,81,109,109	0
2	NAG	A	501	14/15	0.84	0.14	-1.32	39,56,70,75	0
2	NAG	A	502	14/15	0.86	0.12	-1.63	42,57,70,71	0
4	MAN	B	507	11/12	0.58	0.28	-	92,113,132,146	0
3	BMA	B	503	11/12	0.87	0.15	-	41,64,80,80	0
4	MAN	A	504	11/12	0.83	0.18	-	44,72,106,130	0
4	MAN	A	506	11/12	0.71	0.23	-	86,103,117,132	0
3	BMA	A	503	11/12	0.93	0.10	-	44,58,65,86	0
8	FUC	B	508	10/11	0.82	0.24	-	82,87,97,107	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.